

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

NOV 05 ZODA

In re Application of

Examiner:

Slobodyansky, I

MARCIREAU ET AL

Art Unit:

1652

Serial No.: **09/744,125**

Filed:

September 17, 2001

Title:

MEKKI-INTERACTING FHA PROTEIN

hereby certify that this correspondence is being transmitted via facsimile to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, care of Art Unit 1646, at 703-305-3014 on

Pate of Deposit

Printed Name of Person Signing Certificate

DECLARATION UNDER 37 CFR § 1.131 OF
PRIOR INVENTION IN A WORLD TRADE ORGANIZATION (WTO) MEMBER

Signature

Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313

Dear Sir:

Christophe Marcireau declares as follows:

1. I am an inventor of the inventions claimed in U.S. Patent Application Serial No. 09/744,125 filed on September 17, 2001 ("the '125 application").

COUNTRY

- 2. Prior to September 10, 1997 I obtained the nucleic acid of SEQ ID NO:1 in France, a WTO member country.
- 3. Prior to September 10, 1997, I translated SEQ ID NO:1 and obtained the amino acid sequence of SEQ ID NO:2 in France, a WTO member country.
- 4. Attached hereto is a machine-generated graph that shows the results of the sequencing of the nucleic acid of SEQ ID NO:1. The sequencing of SEQ ID

NO:1 and its translation to obtain the amino acid sequence of SEQ ID NO:2 was performed under my direction. The machine-generated date on the graph has been redacted, but that date is prior to September 10, 1997. The sequencing was conducted in France, a WTO member country.

5. I declare that all of the foregoing statements are true, recognizing that willful false statements are punishable by fine or imprisonment, or both, under 18 U.S.C. § 1001, and that any such willful false statements may jeopardize the validity of the application or any patent that issues from it.

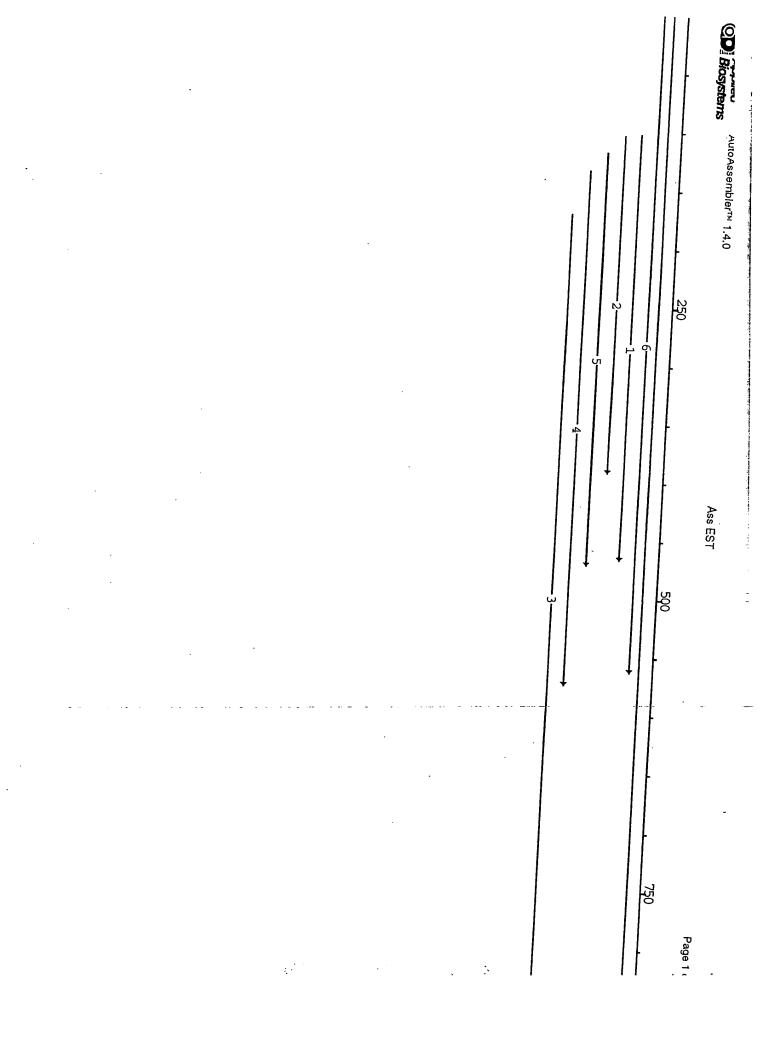
Date: October the 12th

Christophe Marcireau

DNA sequence 1603 b.p. GTGGATCCCCCG ... TCGCCCTATAGT linear

4909+8855+8955+8856+6196 mekk1bp3

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1/1
 GTG GAT CCC CCG GGC TGC AGG AAT TCG GCA CGA GGT GGG GTG GAA CCA GGG CGC TGT TCG
 V D P P G C R N S A R G G V E P G R C S
                              91/31
GGG AGT GAA CCC TCC TCC AGT GAG AAA AAG AAG GTA TCC AAA GCC CCC AGC ACT CCT GTG
G S E P S S S E K K K V S K A P S T P
121/41
                              151/51
CCA CCC AGC CCA GCC CCT GGA CTC ACC AAG CGT GTG AAG AGT AAA CAG CCA
P P S P A P A P G L T K R V K K S K Q P
181/61
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CTT CAG GTG ACC AAG GAT CTG GGC CGC TGG AAG CCT GCA AAT GAC CTC CTG CTC ATA AAT
LQVTKDLGRWKPANDLLL
                              271/91
GCT GTG TTG CAG ACC AAC GAC CTG ACC TCC GTC CAC CTG GGC GTG AAA TTC AGC TGC CGC
     L Q T N D L T S V H L G V K F S C
301/101
                              331/111
TTC ACC CTT CGG GAG GTC CAG GAG CGT TGG TAC GCC CTG CTC TAC GAT CCT GTC ATC TCC
F T L R E V Q E R W Y A L L Y D P V I S
361/121
                              391/131
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K L A C Q A M R Q L H P E A I A A I
421/141
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AAG GCC CTG TTT AGC AAG GCT GAG GAG CAG CTG CTG AGC AAA GTG GGA TCG ACC AGC CAG
K A L F S K A E E Q L L S K V G S T S Q
481/161
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CCC ACC TTG GAG ACC TTC CAG GAC CTG CTG CAC AGA CAC CCT GAT GCC TTC TAC CTG GCC
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541/181
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CGT ACC GCG AAG GCC CTG CAG GCC CAC TGG CAG CTC ATG AAG CAG TAT TAC CTG CTG GAG
R T A K A L Q A H W Q L M K Q Y Y L L E
601/201
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D Q T V Q P L P K G D Q V L N F S D A E
661/221
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D L I D D S K L K D M R D E V L E H E L
                             751/251
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M V A D R R Q K R E I R Q L E Q E L H K
781/261
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841/281
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901/301
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AAT GAG GGT CGA CGC CCC ATC TAC ATC GAT GGA CGG CCG GTG CTC TGT GGC TCC AAA TGG
N E G R R P I Y I D G R P V L C G S K W 1081/361
CGC CTC AGC AAC AAC TCT GTG GTG GAG ATC GCC AGC CTG CGA TTC GTC TTC CTT ATC AAC
RLSNNSVVEIASLRFVFLIN
                             1171/391
CAG GAC CTC ATT GCC CTC ATC AGG GCT GAG CTG CCA AGA TCA CAC CAC AGT GAG GAA TGG
Q D L I A L I R A E L P R S H H S E E W
1201/401
                             1231/411
TGG CAG GAC TCG TGG GCC CTC TCC GGC CTG TTT CCC CTG CCA CTC CAG CCC CCT TGA
W Q D S W A L S G L F P L P L Q P P
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Project: Last saved:

Last assembled:

Ass EST

16:09:01 16:09:55

Threshold: 10.0 Error Rate: 5.0%

O Tolerance: 1 Hit Count: 10 Overlap: 10% 13 Offset: Window:

Total in project: Total in assemblages: Total unassembled: Total dye primer: Total dye terminator: Non-373 sequences:	Sequences 6 6 0 0 0 6	Bases 2576 2576 0 0 2666	Percent 100.0% 100.0% 0.0% 0.0% 0.0% 103.5%	
w26888.Assemblage.1	Sequences 6	Bases 831	Score 1773.0	Ambiguities 34

w26888.Assembl Redundancy Sequence Len		Sequenc Average Average	::	6 B 3.2 H 429 H	_	831 Score 6 Low: 640 Low:	e: 1773.0 1 282
File w26888 aa134651 f12127 w00383 t66207 r52839	Sample	-> -> -> ->	ID 6 1 2 5 4 3	Begin 0 103 104 119 135 172	End 562 467 392 472 575 831	Length 535 352 282 347 420 640	Date Chemistry 12/03/97 12/03/97 12/03/97 12/03/97 12/03/97 12/03/97

0 Sequences: 0 Bases: Unassembled Sequences ID Begin End Sample File

Length

Date Chemistry

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AutoAssembler™ 1.4.0

S MBPS XS

26888. Assemblage. 1 GennnnTACCCAGGACGGACCCTCCAGAGACAGGTCCACATCAATCTGGTTATCCTTGGTTGCTCTGCCCAGGGTGATCTCACGCGAGCGCATCAGGTACCGCAGGGAAGCCGGCTTT~G ACGGAAGCCGGCTTT-G CGGAAGCGNNCTTTTG 26888. Assemblage. 1 CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTGGACTGTAAGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAGGCACT~GCCAGCCG~CTCA~GAG CCTCCTAGCCCGGTGGTTTGGAÅCCAGTGGCTTTTGGAACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCTTGATGGNATCAGGCACT-GCCAGNCG-CTCAAGAG CCTCCTAGCCCTGTGGTTTGGAÅCCAGTGGCTTTTGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCTGATGGCATCAGGCACT-GCCAGCCNGCTCA-GAG cctcctagcccggtggtttggaaccagtggcttttggaactgtnagaggatggacaaagattctnaggggctgctagattcatccctgatggcatcaggcact-gccagccg-ctca-gag CCTCCTAGCCCTGTGGTTTGGAACCAGTGGCTTTGGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCTGATGGCATCAGGCACTTGCAGCCG-CTCAAGAG CCTCCTAGCCCGGTGGTTTGGAÅCCAGTGGCTTTTGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAGGCACT-GC-AGCCG-CTCA-GAG CCTCCTAGCCCGGTGGTTTGGAÅCCAGTGGCTTTTNGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAGGCACT-GCCAGCCG-CTCA-GAG GCCCTGCGGCTGCTACCGTCGNCGAGAAATTGTTGGNTCTGGCAGTCTAGGAATGANTCTCCTCTCAGCNTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCTTT GCC-TGCGGCTGCTACCGTCGCCGGAGAAATTGTTGGANCTGGCAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCTT ccgtcgcc/-cggagaaattgttggatctggcagtctaggaatgaatctcctctctagcctttaagctcacctggtcagaatccttggatgagcctgtgggaccgtt 26888.Assemblage.1 GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTTCC-TCCCA-GGCCTTGGG-a-CCATCC-GGAGAA-GCTCCTCCAa'GGT-CATCAAGAGGAAGAAGTtC-GaTGAT GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTCC-TCCCA-GGCCTTGGG-A-CCATCCC-TAAAC-GGAGAA-GCTCCTCCAGGTT-TATCAAGAGGAAGAAGTTC-GATGAT GATGAGGAGTCACTGGCAGGGCA-GAA-GC-GA-GCCTCC-TCCCA-GGCCTTGGGCA-CCATCCC-TAAAC-GGAGAA-GCTCCTCCAGGTT-CATCAAGAGGAAGAAGTTC-GATGAT GCCCTGCGGCTGCTACCGTCGCCGCAGAAATTGTTGGATCTGGNAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACGNT GGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGTT GATGAGGAGTCACTGGCAGGGNÅ-GAA-GC-GA-GCCTCCCTCCCA-GGCCTTGGG-NACCATCCCCTAAAC-GGAGAA-GNTCCTCCCAGGT-CANCAAGAGGA-GAAGT-CCGNTGAT GATGAGGAGTCACTGGCAGGGCAAGAAAGC-GAAGCCTCC-TCCCAAGGCCTTNGG-A-CCAATCCCTAAACCGGAGAAAGCTCCTCCAAGGTTCATCAAGAGGAAGNAGTT GATGAGGAGTCACTGGCAGGGCÅ-GAA~GCCGA-GCCTCC~TCCCAAGGCCTTGGG-CACCATCCC-TAAAC-GGAGAA-GCTCCTCCAAGGTTCATCAAGAGGAAG GATGAGGAGTCACTGGCAGGGCA-GAA-GN-G Ŷ Ŷ ^ ^ **?** ? Ŷ Ŷ Ŷ **?** ? Ŷ Ŷ Ŷ a134651 a134651 a134651 a134651 v26888 12127 **400383** 52839 66207 52839 52839 ,00383 :66207 12127 200383 12127 26888 26888 12127 700383

OD Biosystems	AutoAssembler™ 1.4.0	untitled 2		Page 2 of 2	e 2 of 2
٠	200	525	550,	575.	009
~26888.Assemblage.1	1 GAGCTGGtGGAGAGCAGCCTGG	#26888.Assemblage.1 GAgcTgGtGGAGAGCCTGGmAAaaTCTtCTtaCCCgGgcAAAGGGGGCCAgt~GGG~tkGAaCCAGGGgcgCTktT~CGGGGAGTGAACCTCCTCCAGTGAAGAAGAAGAAGTATT	KGAaCCAGGGgcgcTktT~CGGGGAGT	GAACCCTCCTCCAGTGAGAAGAAGAAGTATT	TĘ.
	CCCC	AAAINI-CII-CCCCGN-AAAGGGG-CAANGGG-NIGACCCAGGGGIINI-CG	KGACCCAGGGGTTNT-CG		
t66207 ->		GAGCTGGTGGAGGAGCCTGGNAAAATCTTCTTACCCGGGCAAAGGGGGCCAGTTGGG-TNGAACCAGGGGCGCTNTTTCGGGGGGTGAACC-T GAGCTGGTGGAGAGCAGCCTGGCAAAATCTTCT-ACCCGGGCAAAGGGGGCCAGT-GGGGTGGAACCAGGG-CGCTGTT-CGGGGGAGTGAACCTCCTCCAGTGAAAAAAT	VGAACCAGGGGCGCTNTTTCGGGGAGT	GAACC-T GAACCCTCCTGGGGAGGAAGAAGTTT	ıTT
	-	625,	debut it me refuse	. 002	
v26888.Assemblage.	1 CCAAAGCCCCCAGCACTCCTGT	v26888. Assemblage. 1 CCAAAGCCCCCAGCACCCAGCCCCAGCCCCAGCCCCTGGGATTCACCAAGCGTGAAAAAAAA	CTGTGAAGAAGAGTAAACAGCCATTT	TCAGGTGAACCAAGGATCTTGGGCCGTTGGAA]ĕ
				•	*
:52839 ->		CCAAAGCCCCCAGCACTCTGTGCCCACCCAGCCCCAGCCCCTGGGATTCACCAAGCGTGTGAAGAAGAGTAAACAGCCATTTTCAGGTGAACCAAGGATCTTGGGCCGTTGGAA	GTGTGAAGAAGAGTAAACAGCCATTT	TCAGGTGAACCAAGGATCTTGGGCCGTTGGAA	AA
1 000 July 2009	725,	777 775	800	825,	
vooco : resedintage :	vaosoo. Assellatage. 1 GC11GCAGA11GANCTICTINITAATTGTTGTTGTT	IATTAAATTGTTGTGTTTGCAGACCAACGACTTAACTTCD:	TGCAGACCAACGACTTAACTTCATTGGGATGAAATTTAAGTTACCGTTTAACCTTTAGGAAGTTCAG	CGTTTAACCTTTnGGAAGTTCAG	

-> GCTTGCAGATTGANCTTCTTNTTATAAATTGTTGTGTTTGCAGACCAACGACTTAACTTCNTTCACTTGGGNTGAAATTTNAGTTNCCGTTTAACCTTTNGGAAGTTCAG :52839

Model 377 Version 2.1.1

22°CM 5

6067

Signal G:406 A:809 T:268 C:303
*DT4%Ac(A Set-AnyPrimer)
S/N 95080645
Points 1207 to 11812 Base 1: 1207

Page 1 of 2 11.23 ABI100

bandane Malderan Indian Kindungan Indian pangkan pengkan pengkan pengkan Indian Pengkal Panghan Late by he minimited I have the little of the man production and work of a long to more production to the production of the produc CM 5 Lane 22



mbp3nt [1 to 1257] -> 1-phase Translation

DNA sequence 1603 b.p. GTGGATCCCCCG ... TCGCCCTATAGT linear

4909+8855+8955+8856+6196 mekk1bp3

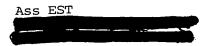
1/1 GTG V 61/	GAT D	CCC P	CCG P	GGC G	TGC C	AGG R	AAT N	TCG S	GCA A		GGT G	GGG G	GTG V	GAA E	CCA P	GGG G	CGC R	TGT C	TCG S
GGG G	AGT S ./41	GAA E	CCC P	TCC S	TCC S	AGT S	GAG E	AAA K	AAG K	AAG K	GTA	TCC S	AAA K	GCC A	CCC P	AGC S	ACT T	CCT P	GTG V
P 181	CCC P /61	s	P	A	P	A	P	G	L	ACC T 211	AAG K /71	R _.	V	K	K	S	K	Q	P
L 241	' CAG Q ./81	V	T	K	D	L	G	R	W	K 271	P /91	A	N	D	L	L	L	I	N
A 301	' GTG V /101	L	Q	Т	N	D	L	T	S	V 331	Н /111	L	G	V	K	F	S	С	R
F 361	ACC T /121	L	R	Е	V	Q	E	R	W	Y 391	A /131	L	L	Y	D	P	V	I	S
К 421	TTG L /141	A	С	Q	A	М	R	Q	L	н 451	P /151	E	A	I	A	A	I	Q	S
K 481	GCC A /161	L	F	S	K	Α	E	E	Q	L 511	L /171	S	K	V	G	S	T	s	Q
P 541	ACC T /181	L	E	T .	F	Q	D	L	L	H 571	R /191	Н	P	D	A	F	Y	L	A
R 601	ACC T /201	A	K	Α .	L	Q	A	Н	W	Q 631,	L /211	M	K	Q	Y	Y	L	L	E
D 661	CAG Q /221 CTG	T	V	Q	P	L	P	K	G	D 691,	Q /231	V	L	N	F	S	D	A	E
D 721	L /241 GTG	I	D	D	S	K	L	ĸ	D	м 751,	R /251	D	E	V	L	E	Н	E	L
м 781,		A	D	R	R	Q	ĸ	R	E	I 811,	R /271	Q	L	E	Q	E	L	H	K
W 841,	Q /281	V	L	V _	D	S	Ι	T	G	M 871,	S /291	S	P	D	F	D	N	Q	T CTG
L 901,		V	L	R	G ≨	R	M	V	R	Y 931/	L /311	M	R	s	R	E	I	T 4	L_
AAG	/321 ATA	TCC					Q GTC			V 991/ CTG	/331	L AAC							W GCC
1021 AAT	I 17341 GAG	GGT	CGĂ)	ccc	ccc	ATC		ATC	GAT	1051 GGA		CCG		CTC	TGT			_	A TGG
CGC	L/361 CTC	AGC	AAC		TCT	GTG (GTG	GAG		1111 GCC		CTG	CGA	TTC	GTC		_		W Aac
1141 CAG	L L/381 GAC	CTC .	ATT	GCC	CTC	ATC .	AGG	GCT	GAG	1171 CTG		AGA	TCA	CAC	CAC	AGT	GAG	GAA	
1201 TGG	D ./401 CAG	GAC '	TCG		GCC ·	CTC 1	rcc ·	GGC	CTG	1231 TTT		CTG	CCA	CTC	CAG	ccc ·	CCT	TGA	W
W	V	D .	S	₩ .	A :	L :	5	G	ь	F	P	L	P	L '	Õ	P	P	*	

Page 1 of 1



Project:

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Threshold: 10.0 Error Rate: 5.0%

0 Tolerance: 1 Hit Count: 10 Overlap: 10% 13 Offset: Window:

Total in project: Total in assemblages: Total unassembled: Total dye primer: Total dye terminator: Non-373 sequences:	Sequences 6 6 0 0 0 6	Bases 2576 2576 0 0 2666	Percent 100.0% 100.0% 0.0% 0.0% 0.0% 103.5%	
Non-3/3 sequences.	·	•		1

Score Ambiguities Bases Sequences 1773.0 6 831 w26888.Assemblage.1

w26888.Assem Redundancy Sequence Lo		Sequenc Average Average	: :	6 H 3.2 H 429 H	-	831 Scor 6 Low: 640 Low:	
File w26888 aa134651 f12127 w00383 t66207 r52839	Sample	-> -> -> ->	ID 6 1 2 5 4 3	Begin 0 103 104 119 135 172	End 562 467 392 472 575 831	Length 535 352 282 347 420 640	Date Chemistry 12/03/97 12/03/97 12/03/97 12/03/97 12/03/97 12/03/97

Unassembled Sequences Sample File

Sequences: ID Begin

0 Bases: End

0 Length

Date Chemistry

MBPS HS

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J	`

Applied AutoAssembler™ 1.4.0 Biosystems

		25	20	75	100
w26888.Assemblage.1	w26888.Assemblage.1 GGnnnnTACCCAGGACGGACCTCCAGAGACAGGTC	CTCCAGAGACAGGTCCACATCAATC	TGGTTATCCTTGGTTGCTCTGCCC	GGGTGATCTCACGCGAGCG	CACATCAATCTGGTTATCCTTGGTTGCTCTGCCCAGGGTGATCTCACGCGAGCGCATCAGGTACCACAAACCAAAAAAAA
w26888> aa134651> f12127> w00383>	GGNNNNTACCCAGGACGGACC	CTCCAGAGACAGGTCCACATCAATC	TGGTTATCCTTGGTTGCTCTGCCCA	GGGTGATCTCACGCGAGCG	GGNNNNTACCCAGGACGCACCTCCAGAGACAGGTCCACATCAGTTTATCCTTTGGTTTGCTCTTGCCCAGGGTGATCTCACGCGAGCGCATCAGGTACCGCACGGAAGCCGGETTTT-G ACGGAAGCCGGCTTTT-G CGGAAGCCGNNCTTTTG G
w26888.Assemblage.1	125 150 A26888.Assemblage.1 GCCcTGCGGCTGCTACCGTCGCGGGAGAATTGT	150 SCCGCGGAGAATTGTTGGATCTGGCA	175 AGTCTAGGAATGAATCTCCTCTCAG	200 SCCTTTAAGCTCACCTGGTC	175 225 TEGATCTGGCAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGTCAGAATCCTTGGATGAGCCTGTGGGACCGTT
#26888 -> aa134651 -> f12127 -> #00383 -> t66207 -> r52839 ->	GCCCTGCGGCTGCTACCGTCGCCGCGGAGAAATTGT GCC-TGCGGCTGCTACCGTCGCCGCGGGAAAATTGT GCC-TGCGGCTGCTACCGTCGNCGNGGAGAAATTGT GCC-TGCGGCTGCTCGCCGCGGAGAAATTGT CCGTCGCC-CGGAGAAATTGT	CCGTCGCCGCAGAAATTGTTGGATCTGGN) CCGTCGCCGCGGAGAAATTGTTGGNTCTGGC) CCGTCGNCGNGGAGAAATTGTTGGNTCTGGC) CCGTCGCCGCGGAGAAATTGTTGGANCTGGC) CCGTCGCC-CGGAGAAATTGTTGGATCTGGC)	AGTCTAGGAATGAATCTCCTCTCAGAGTCTGCTCTCAGAGTTGAATCTCCTCTCTCAGAGTTGANTCTCCTCTCAGAGTCTGCTCTCAGAGTGAATGAATCTCCTCTCAGAGTGAATGAA	SCTTTAAGCTCACCTGGTC) SCTTTAAGCTCACCTGGTC) SCTTTAAGCTCACCTGGTC) SCCTTTAAGCTCACCTGGTC) SCCTTTAAGCTCACCTGGTC)	GCCTGCGGCTGCTACCGTCGCCGGAGAAATTGTTGGATCTGGNAGTCTAGGAATGAATCTCCTCTCAGCCTTTAAGCTCACCTGGAAATCCTTGGATGAGCCTGTGGGACCGNT GCCTGCGGCTGCTACCGTCGCGGAGAAATTGTTGGATCTCTGGCAGTCTAGGAATGAAT
w26888.Assemblage.1	250 CCTCCTAGCCCgGTGGTTTTGC	275 SAACCAGTGGCTTTGGGACTGTAAGA	300 GGATGGACAAAGATTCTCAGGGGCT	325 :GCTAGATTCATCCTGATG	250 350 350 350 350 350 350 350 350 325 350 350 325 350 350 350 350 350 350 350 350 350 35
w26888 -> aa134651 -> f12127 -> w00383 -> t66207 ->	CCTCCTAGCCCGGTGGTTTGC CCTCCTAGCCCGGTGGTTTTGC CCTCCTAGCCCGGTGGTTTTGC CCTCCTAGCCCGGTGGTTTTGC	BAACCAGTGGCTTTGGGACTGTAAGA BAACCAGTGGCTTTGGGACTGTNAGA BAACCAGTGGCTTTGGGACTGTNAGA BAACCAGTGGCTTTGGGACTGTAAGA BAACCAGTGGCTTTTGGGACTGTAAGA	GGATGGACAAAGATTCTCAGGGGCT GGATGGACAAAGATTCTNAGGGGCT GGATGGACAAAGATTCTNAGGGGCT GGATGGACAAAGATTCTCAGGGGCT GGATGGACAAAGATTCTCAGGGGCT	ICTAGATTCATCCCTGATG ICCTAGATTCATCCCTGATG ICCTAGATTCATCCCTGATG ICCTAGATTCATCCCTGATG ICCTAGATTCATCCCTGATG ICCTAGATTCATCCCTGATG	CCTCCTAGCCCGGTGGTTTGGAACCAGTGGCTTTTGGACTGTAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGNATCAGGCACT-GCCAGNCG-CTCAAGAG CCTCCTAGCCCGGTGGTTTTGGAACCAGTGGCTTTTGGAACTGTTAAAGAGATGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATCAGGCACT-GCCAGCCG-CTCA-GAG CCTCCTAGCCCGGTGGTTTTGGAACCAGTGGCTTTTGGAACTGTAAAGAGATGAACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCACTTGCAGCCCTCTAAGAG CCTCCTAGCCCGGTGGTTTTGGAACCAGTGGCTTTTGGAACTGTAAAGAGGATGGACAAAGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATTAGGAACCAGTGGCTTTTGGAACTGTAAAGAGGATTCTCAGGGGCTGCTAGATTCATCCCTGATGGCATTAGGAACCAGTGGCTTTTNGGACTGTAAAGAGGATTGCACAAAGATTCTCAGGGGCTTCAAGATCCTAGATTCATCCTTGATGGCATTTGGAACCAGTGGCTTTNGGACTGTAAAGATGCAAAAGATTCTCAGGGGCTTCAAGATTCATCATCGCATCATAGGACTTTNGGACTGTAAGAGGATTGGACAAAGATTCTCAGGGGCTTCAAGATTCATCATCGTAAGAGTTCATCATGGAACCAGTGGCTTTTNGGACTTGTAAGAGGATTGCACAAAGATTCTCAGGGGCTTCAAGATTCATCATCATGCAATCAAGACCAGTGGCTTTTNGGACTTGTAAAGAGGATTCTCCAGGGCCTGCTAGATTCATCATTCAT
w26888.Assemblage.1	375 w26888.Assemblage.1 GATGAGGAGTCACTGGCAGGGCA~GAA~GC~GA~GC		425 -GGCCTTGGG-a-CCATCC-TAAP	450 AC~GGAGAA~GCTCCTCCAA	400 475 450 475 CTCC~TCCA~GGCCTTGGG~a~CCATCCAGGGAA~GCTCCTCCAAGGT~CATCAAGAGGAAGAAGTtC~GaTGAT
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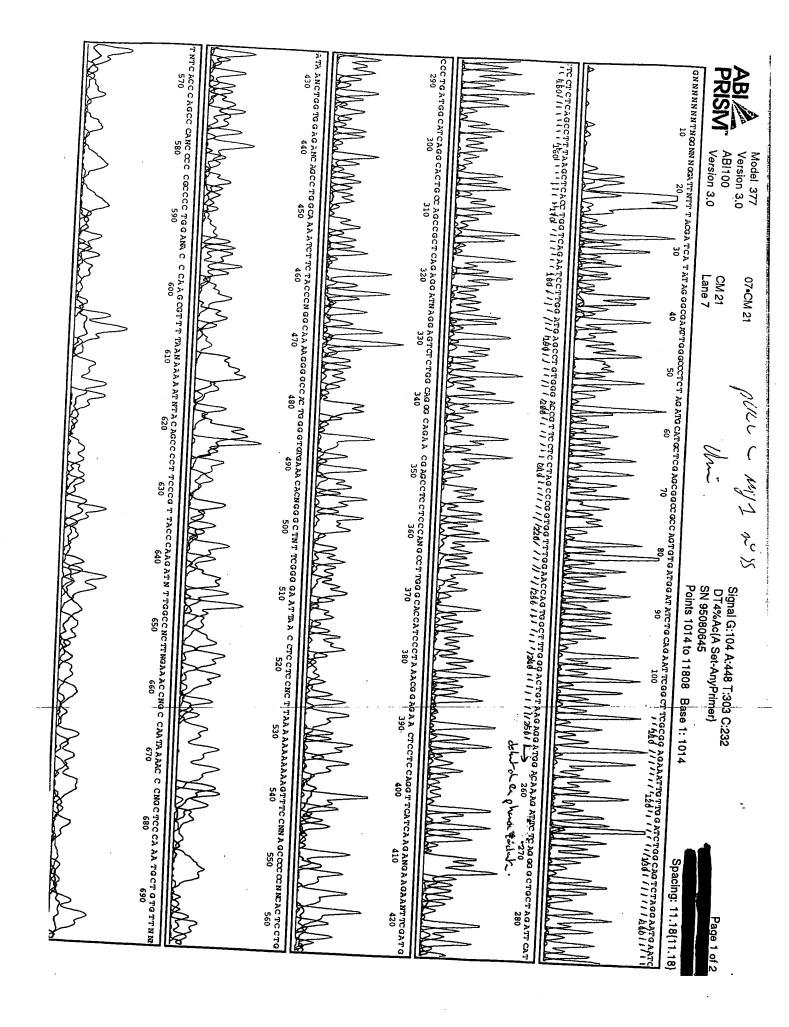
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